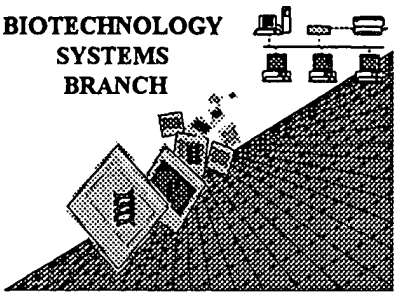
A. Davenport

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/003,869

Art Unit / Team No. : 1654

Date Processed by STIC: 8/16/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED **SUGGESTED CORRECTION** SERIAL NUMBER: 09/003,869

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 ____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 ____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 ____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 ____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 ✓ Variable Length
Sequence(s) 4 contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 ____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.

8 ____ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 ____ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ____ Use of **n's** or **Xaa's** (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

11 ____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 ____ Use of <220>Feature (NEW RULES)
Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Pleas explain sourc of genetic material in <220> t <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 ____ PatentIn ver. 2.0 "bug"
Please do not use "Copy t Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/003,869

DATE: 08/16/1999
TIME: 13:40:00

Input Set: I003869.RAW

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

Does Not Comply
Corrected Diskette Needed

```
1   <110> BEELEY, NIGEL ROBERT ARNOLD
2         PRICKETT, KATHRYN S.
3         BHAVSAR, SUNIL
4   <120> USE OF EXENDINS AND AGONISTS THEREOF FOR
5         THE REDUCTION OF FOOD INTAKE
6   <130> 231/181
7   <140> US/09/003,869
8   <141> 1998-01-07
9   <150> US 60/034,905
10  <151> 1997-01-07
11  <150> US 60/055,404
12  <151> 1997-08-08
13  <150> US 60/065,442
14  <151> 1997-11-14
15  <150> US 60/066,029
16  <151> 1997-11-14
17  <160> 188
18  <170> FastSEQ for Windows Version 3.0
```

ERRORED SEQUENCES FOLLOW

```
19  <210> 4
20  <211> 29
21  <212> PRT
22  <213> Artificial Sequence
23  <220>
24  <223> artificially synthesized sequence of novel exendin agonist
25        compound
26  <220>
27  <221> VARIANT
28  <222> (1)...(7)
29  <223> Xaa in position 1 is His, Arg or Tyr; Xaa in position 2 is
30        Ser, Gly, Ala or Thr; Xaa in position 3 is Asp or Glu;
31        Xaa in position 5 is Ala or Thr; Xaa in position 6 is Ala,
32        Phe, Tyr or naphthylalanine; Xaa in position 7 is Thr or Ser;
33  <220>
34  <221> VARIANT
35  <222> (8)...(13)
36  <223> Xaa in position 8 is Ala, Ser or Thr; Xaa in position 9 is
37        Asp or Glu; Xaa in position 10 is Ala, Leu, Ile, Val, pentyl-
38        glycine or Met; Xaa in position 11 is Ala or Ser; Xaa in
39        position 12 is Ala or Lys; Xaa in position 13 is Ala or Gln;
```

FYI:

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

```
<220>
<221> VARIANT
<222> (14)...(20)
<223> Xaa in position 14 is Ala, Leu, Ile, pentylglycine, Val or
      Met; Xaa in position 15 is Ala or Glu; Xaa in position 16 is
      Ala or Glu; Xaa in position 17 is Ala or Glu; Xaa in position
      19 is Ala or Val; Xaa in position 20 is Ala or Arg;
<220>
<221> VARIANT
<222> (21)...(24)
<223> Xaa in position 21 is Ala or Leu; Xaa in position 22 is Ala,
      Phe, Tyr or naphthylalanine; Xaa in position 23 is Ile, Val,
      Leu, pentylglycine, tert-butylglycine or Met; Xaa in position
      24 is Ala, Glu or Asp;
<220>
<221> VARIANT
<222> (25)...(28)
<223> Xaa in position 25 is Ala, Trp, Phe, Tyr or naphthylalanine;
      Xaa in position 26 is Ala or Leu; Xaa in position 27 is Ala
      or Lys; Xaa in position 28 is Ala or Asn;
<220>
<221> VARIANT
<222> (29)...(29)
<223> Xaa in position 29 is -OH; -NH2; Gly-Z2; Gly Gly-Z2; Gly Gly
      Xaa31-Z2; Gly Gly Xaa31 Ser-Z2; Gly Gly Xaa31 Ser Ser-Z2; Gly Gly
      Xaa31 Ser Ser Gly-Z2; Gly Gly Xaa31 Ser Ser Gly Ala-Z2; Gly Gly
      Xaa31 Ser Ser Gly Ala Xaa36-Z2;
<220>
<221> VARIANT
<222> (29)...(29)
<223> Gly Gly Xaa31 Ser Ser Gly Ala Xaa36 Xaa37-Z2; or Gly Gly Xaa31
      Ser Ser Gly Ala Xaa36 Xaa37 Xaa38-Z2;
<220>
<221> VARIANT
<222> (29)...(29)
<223> where Xaa31, Xaa36, Xaa37 and Xaa38 are independently Pro,
      homoproline, 3-hydroxyproline, 4-hydroxyproline, thioproline,
      N-alkylglycine, N-alkylpentylglycine or N-alkylalanine;
      and Z2 is -OH or -NH2;
<220>
<221> VARIANT
<222> (3)...(28)
<223> provided that no more than three of Xaa in positions 3, 5, 6,
      8, 10, 11, 12, 13, 14, 15, 16, 17, 19, 20, 21, 24, 25, 26,
      27 and 28 are Ala.
<400> 4
W--> Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
E--> 1               5                  10                  15
W--> Xaa Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                20                  25
```

see item 6 on Error Summary Sheet.

Xaa can only represent a single amino acid, nothing else

? Only 29 amino acids are shown in the sequence

Then mention Ala in (223) for position 3 (see p. 1)

(1) Move numbers

(20) Under amino acid

Please number amino acids UNDER every 5 amino acids.
DO NOT use TAB codes between amino acid numbers; use space

VERIFICATION SUMMARY
PATENT APPLICATION **US/09/003,869**

Input Set: **I003869.RAW**

Line	?	Error/Warning	Original Text
86	W	"N" or "Xaa" used: Feature required	Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa X
87	E	Invalid/Missing Amino Acid Numbering	
88	W	"N" or "Xaa" used: Feature required	Xaa Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X